

## SEQUENCE LISTING

<110> Williamson, Richard

Burn, Joanne

<120> Methods and means for modulating cellulose biosynthesis in fiber producing plants

<130> BCS 02 2001

<150> US 60/432,674

<151> 2002-12-12

<160> 23

<170> PatentIn version 3.1

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<212> DNA

<213> Arabidopsis thaliana

<220>

<221> misc\_feature

<222> (121)..(1986)

<223> coding RSW2

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<213> Artificial Sequence

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<223> cDNA RSW2 homologue from cotton

<220>

<221> misc\_feature

<222> (47)..(1906)

<223> coding region RSW2 homologue

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&lt;212&gt; DNA

<213> *Arabidopsis thaliana*

&lt;400&gt; 3

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<221> misc\_feature

<222> (2)..(1576)

<223> C-terminal part of the coding region

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Leu Gly Pro Thr Glu Gln Lys Lys Lys Lys Tyr Val Asp Leu Gly Cys
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Ile Ile Val Ser Arg Lys Ile Phe Val Trp Thr Val Gly Thr Leu Val
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 130 135 140

Gly Lys Gly Glu Thr Gly Ser Phe Tyr Lys Asp Leu Val Gly Gly Tyr  
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Met Thr Met Leu Ser Trp Ser Val Ile Glu Tyr Ser Ala Lys Tyr Glu  
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Ala Ala Gly Glu Leu Thr His Val Lys Glu Leu Ile Lys Trp Gly Thr  
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Asp Tyr Phe Leu Lys Thr Phe Asn Ser Thr Ala Asp Ser Ile Asp Asp  
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Ile	Glu	Gly	Ala	Met	Val	Ala	Gly	Pro	Asp	Lys	Arg	Asp	Gly	Tyr	Arg	
545					550					555					560	

Asp Val Arg Met Asn Tyr Asn Tyr Thr Glu Pro Thr Leu Ala Gly Asn  
                   565                                  570                                  575

Ala Gly Leu Val Ala Ala Leu Val Ala Leu Ser Gly Glu Glu Glu Ala  
                   580                                  585                                  590

Thr Gly Lys Ile Asp Lys Asn Thr Ile Phe Ser Ala Val Pro Pro Leu  
                   595                                  600                                  605

Phe Pro Thr Pro Pro Pro Pro Pro Ala Pro Trp Lys Pro  
           610                                  615                                  620

<210> 6

<211> 619

<212> PRT

<213> cotton

<400> 6

Met Tyr Gly Arg Asp Pro Trp Gly Gly Pro Leu Glu Ile Asn Ala Thr  
   1                  5                                  10                                  15

Asp Ser Ala Thr Asp Asp Asp Arg Ser Arg Asn Leu Gln Asp Leu Asp  
                   20                                  25                                  30

Arg Ala Ala Leu Ser Arg Pro Leu Asp Glu Thr Gln Gln Ser Trp Leu  
                   35                                  40                                  45

Leu Gly Pro Gly Glu Gln Lys Lys Lys Lys Tyr Val Asp Leu Gly  
   50                                  55                                  60

Cys Ile Ile Val Ser Arg Lys Ile Phe Val Trp Thr Val Gly Thr Leu  
   65                  70                                  75                                  80

Leu Val Ser Ala Leu Leu Ala Gly Leu Ile Thr Leu Ile Val Lys Thr  
                   85                                  90                                  95

Val Pro Arg His His His Arg His Ser Pro Pro Asp Asn Tyr Thr Leu  
                   100                                  105                                  110

Ala Leu His Lys Ala Leu Met Phe Phe Asn Ala Gln Arg Ser Gly Lys  
 115 120 125

Leu Pro Lys His Asn Asn Val Ser Trp Arg Gly Asn Ser Gly Leu Gln  
 130 135 140

Asp Gly Lys Ser Asp Pro Ser Val Leu Met Lys Asp Leu Val Gly Gly  
 145 150 155 160

Tyr Tyr Asp Ala Gly Asp Ala Ile Lys Phe Asn Phe Pro Ala Ser Phe  
 165 170 175

Ser Met Thr Met Leu Ser Trp Ser Val Ile Glu Tyr Ser Ala Lys Tyr  
 180 185 190

Glu Ala Ala Gly Glu Leu Asn His Val Lys Glu Ile Ile Lys Trp Gly  
 195 200 205

Thr Asp Tyr Leu Leu Lys Thr Phe Asn Asn Thr Ala Asp Thr Ile Asp  
 210 215 220

Arg Ile Ala Ala Gln Val Gly Ile Gly Asp Thr Ser Gly Gly Ser Ser  
 225 230 235 240

Ala Pro Asn Asp His Tyr Cys Trp Met Arg Pro Glu Asp Ile Asp Tyr  
 245 250 255

Pro Arg Pro Val Tyr Glu Cys His Ser Cys Ser Asp Leu Ala Ala Glu  
 260 265 270

Met Ala Ala Ala Leu Ala Ser Ala Ser Ile Val Phe Lys Asp Asn Lys  
 275 280 285

Ala Tyr Ser Gln Lys Leu Val His Gly Ala Arg Thr Leu Phe Met Phe  
 290 295 300

Ala Arg Asp Gln Arg Gly Arg Tyr Ser Ala Gly Gly Ser Asp Pro Ala  
 305 310 315 320

Leu Phe Tyr Asn Ser Ser Ser Tyr Trp Asp Glu Phe Val Trp Gly Gly  
 325 330 335

Ala Trp Leu Tyr Tyr Ala Thr Gly Asn Ser Ser Tyr Leu Gln Leu Ala  
 340 345 350

Thr His Pro Lys Leu Ala Lys His Ala Gly Ala Phe Trp Gly Gly Pro  
 355 360 365

Asp Tyr Gly Val Leu Ser Trp Asp Asn Lys Leu Ala Gly Ala Gln Val  
 370 375 380

Leu Leu Ser Arg Leu Arg Leu Phe Leu Ser Pro Gly Tyr Pro Tyr Glu  
 385 390 395 400

Glu Ile Leu Ser Thr Phe His Asn Gln Thr Ser Ile Ile Met Cys Ser  
 405 410 415

Phe Leu Pro Val Phe Thr Ser Phe Asn Arg Thr Lys Gly Gly Leu Ile  
 420 425 430

Gln Leu Asn His Gly Arg Pro Gln Pro Leu Gln Tyr Val Val Asn Ala  
 435 440 445

Ala Phe Leu Ala Ala Leu Tyr Ser Asp Tyr Leu Asp Thr Ala Asp Thr  
 450 455 460

Pro Gly Trp Tyr Cys Gly Pro Asn Phe Tyr Ser Thr Asp Val Leu Arg  
 465 470 475 480

Glu Phe Ala Lys Thr Gln Ile Asp Tyr Ile Leu Gly Lys Asn Pro Arg  
 485 490 495

Lys Met Ser Tyr Val Val Gly Phe Gly Asn His Tyr Pro Lys His Val  
 500 505 510

His His Arg Gly Ala Ser Ile Pro Lys Asn Lys Ile Lys Tyr Asn Cys  
 515 520 525

Lys Gly Gly Trp Lys Trp Arg Asp Thr Ser Lys Pro Asn Pro Asn Thr  
 530 535 540

Leu Val Gly Ala Met Val Ala Gly Pro Asp Lys His Asp Gly Phe Arg  
 545 550 555 560

Asp Val Arg Thr Asn Tyr Asn Tyr Thr Glu Pro Thr Leu Ala Gly Asn

565

570

575

Ala Gly Leu Val Ala Ala Leu Val Ala Leu Ser Gly Asp Lys Ala Thr  
                   580                                  585                                  590

Val Ile Asp Lys Asn Thr Ile Phe Ser Ala Val Pro Pro Met Phe Pro  
                   595                                  600                                  605

Thr Pro Pro Pro Pro Pro Ala Pro Trp Lys Pro  
           610                                  615

&lt;210&gt; 7

&lt;211&gt; 921

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 7

Met Arg Ser Leu Leu Phe Val Leu Ser Leu Ile Cys Phe Cys Ser Gln  
   1                  5                                  10                                  15

Thr Ala Leu Ser Trp Lys Lys Glu Glu Phe Arg Ser Cys Asp Gln Thr  
                   20                                  25                                  30

Pro Phe Cys Lys Arg Ala Arg Ser Arg Thr Pro Gly Ala Cys Ser Leu  
                   35                                  40                                  45

Ile Val Gly Asp Val Ser Ile Thr Asp Gly Asp Leu Val Ala Lys Leu  
           50                                  55                                  60

Leu Pro Lys Ala Pro Asn Gln Gly Asp Gly Asp Gln Ile Lys Pro Leu  
   65                                  70                                  75                                  80

Ile Leu Ser Leu Ser Val Tyr Lys Asp Gly Ile Val Arg Leu Lys Ile  
                   85                                  90                                  95

Asp Glu Asp His Ser Leu Asn Pro Pro Lys Lys Arg Phe Gln Val Pro  
                   100                                  105                                  110

Asp Val Val Val Ser Glu Phe Glu Glu Lys Lys Ile Trp Leu Gln Lys  
           115                                  120                                  125

Val Ala Thr Glu Thr Ile Ser Gly Asp Thr Ser Pro Ser Ser Val Val  
 130 135 140

Tyr Val Ser Asp Gly Tyr Glu Ala Val Val Arg His Asp Pro Phe Glu  
 145 150 155 160

Val Tyr Val Arg Glu Lys Ser Gly Asp Arg Arg Arg Val Val Ser Leu  
 165 170 175

Asn Ser His Gly Leu Phe Asp Phe Glu Gln Leu Gly Arg Lys Thr Glu  
 180 185 190

Gly Asp Asn Trp Glu Glu Lys Phe Arg Thr His Thr Asp Ser Arg Pro  
 195 200 205

Ser Gly Pro Gln Ser Ile Ser Phe Asp Val Ser Phe Tyr Asp Ser Ser  
 210 215 220

Phe Val Tyr Gly Ile Pro Glu His Ala Thr Ser Phe Ala Leu Lys Pro  
 225 230 235 240

Thr Lys Gly Pro Gly Val Glu Glu Ser Glu Pro Tyr Arg Leu Phe Asn  
 245 250 255

Leu Asp Val Phe Glu Tyr Asp His Glu Ser Pro Phe Gly Leu Tyr Gly  
 260 265 270

Ser Ile Pro Phe Met Val Ser His Gly Lys Ser Gly Lys Thr Ser Gly  
 275 280 285

Phe Phe Trp Leu Asn Ala Ala Glu Met Gln Ile Asp Val Leu Ala Asn  
 290 295 300

Gly Trp Asp Ala Glu Ser Gly Ile Ser Leu Pro Ser Ser His Ser Arg  
 305 310 315 320

Ile Asp Thr Phe Trp Met Ser Glu Ala Gly Ile Val Asp Thr Phe Phe  
 325 330 335

Phe Val Gly Pro Glu Pro Lys Asp Val Val Lys Gln Tyr Ala Ser Val  
 340 345 350



Thr Gly Thr Ser Ala Met Pro Gln Leu Phe Ala Thr Gly Tyr His Gln  
 355 360 365

Cys Arg Trp Asn Tyr Lys Asp Glu Glu Asp Val Ala Gln Val Asp Ser  
 370 375 380

Lys Phe Asp Glu His Asp Ile Pro Tyr Asp Val Leu Trp Leu Asp Ile  
 385 390 395 400

Glu His Thr Asp Gly Lys Arg Tyr Phe Thr Trp Asp Ser Val Leu Phe  
 405 410 415

Pro His Pro Glu Glu Met Gln Lys Lys Leu Ala Ala Lys Gly Arg Lys  
 420 425 430

Met Val Thr Ile Val Asp Pro His Ile Lys Arg Asp Asp Ser Tyr Phe  
 435 440 445

Leu His Lys Glu Ala Thr Gln Met Gly Tyr Tyr Val Lys Asp Ser Ser  
 450 455 460

Gly Lys Asp Phe Asp Gly Trp Cys Trp Pro Gly Ser Ser Ser Tyr Ile  
 465 470 475 480

Asp Met Leu Ser Pro Glu Ile Arg Lys Trp Trp Gly Gly Arg Phe Ser  
 485 490 495

Tyr Lys Asn Tyr Val Gly Ser Thr Pro Ser Leu Tyr Thr Trp Asn Asp  
 500 505 510

Met Asn Glu Pro Ser Val Phe Asn Gly Pro Glu Val Thr Met Pro Arg  
 515 520 525

Asp Ala Leu His Val Gly Gly Val Glu His Arg Glu Val His Asn Ala  
 530 535 540

Tyr Gly Tyr Tyr Phe His Met Ala Thr Ser Asp Gly Leu Val Met Arg  
 545 550 555 560

Glu Glu Gly Lys Asp Arg Pro Phe Val Leu Ser Arg Ala Ile Phe Pro  
 565 570 575

Gly Thr Gln Arg Tyr Gly Ala Ile Trp Thr Gly Asp Asn Thr Ala Glu  
 580 585 590

Trp Glu His Leu Arg Val Ser Ile Pro Met Ile Leu Thr Leu Gly Leu  
 595 600 605

Thr Gly Ile Thr Phe Ser Gly Ala Asp Ile Gly Gly Phe Phe Gly Asn  
 610 615 620

Pro Glu Pro Glu Leu Leu Val Arg Trp Tyr Gln Val Gly Ala Tyr Tyr  
 625 630 635 640

Pro Phe Phe Arg Gly His Ala His His Asp Thr Lys Arg Arg Glu Pro  
 645 650 655

Trp Leu Phe Gly Glu Arg Asn Thr Glu Leu Met Arg Asp Ala Ile His  
 660 665 670

Thr Arg Tyr Thr Leu Leu Pro Tyr Phe Tyr Thr Leu Phe Arg Glu Ala  
 675 680 685

Asn Val Thr Gly Val Pro Val Val Arg Pro Leu Trp Met Glu Phe Pro  
 690 695 700

Gln Asp Glu Ala Thr Phe Ser Asn Asp Glu Ala Phe Met Val Gly Ser  
 705 710 715 720

Gly Leu Leu Val Gln Gly Val Tyr Thr Lys Gly Thr Thr Gln Ala Ser  
 725 730 735

Val Tyr Leu Pro Gly Lys Glu Ser Trp Tyr Asp Leu Arg Asn Gly Lys  
 740 745 750

Thr Tyr Val Gly Gly Lys Thr His Lys Met Asp Ala Pro Glu Glu Ser  
 755 760 765

Ile Pro Ala Phe Gln Lys Ala Gly Thr Ile Ile Pro Arg Lys Asp Arg  
 770 775 780

Phe Arg Arg Ser Ser Ser Gln Met Asp Asn Asp Pro Tyr Thr Leu Val  
 785 790 795 800

Val Ala Leu Asn Ser Ser Gln Glu Ala Glu Gly Glu Leu Tyr Ile Asp

	805		810		815
Asp Gly Lys Ser Phe Glu Phe Arg Arg Gly Ser Tyr Ile His Arg Arg	820		825		830
Phe Val Phe Ser Lys Gly Val Leu Thr Ser Thr Asn Leu Ala Pro Pro	835		840		845
Glu Ala Arg Leu Ser Ser Gln Cys Leu Ile Asp Arg Ile Ile Leu Leu	850		855		860
Gly His Ser Ser Gly Pro Lys Ser Ala Leu Val Glu Pro Leu Asn Gln	865		870		875
Lys Ala Glu Ile Glu Met Gly Pro Leu Arg Met Gly Gly Leu Val Ala	885		890		895
Ser Ser Gly Thr Lys Val Leu Thr Ile Arg Lys Pro Gly Val Arg Val	900		905		910
Asp Gln Asp Trp Thr Val Lys Ile Leu	915		920		

&lt;210&gt; 8

&lt;211&gt; 524

&lt;212&gt; PRT

&lt;213&gt; cotton

&lt;400&gt; 8

Tyr Asp Val Leu Trp Leu Asp Ile Glu His Thr Asp Gly Lys Arg Tyr	1	5	10	15
Phe Thr Trp Asp Lys Met Leu Phe Pro His Pro Glu Glu Met Gln Arg	20	25	30	
Lys Leu Ala Ala Lys Gly Arg His Met Val Thr Ile Val Asp Pro His	35	40	45	
Ile Lys Arg Asp Glu Ser Phe His Leu His Lys Asp Ala Ser Gln Arg	50	55	60	

Gly Tyr Tyr Val Lys Asp Ala Thr Gly Lys Asp Tyr Asp Gly Trp Cys  
65 70 75 80

Trp Pro Gly Ser Ser Ser Tyr Pro Asp Met Leu Asn Pro Glu Ile Arg  
85 90 95

Ser Trp Trp Ala Glu Lys Phe Ser Tyr Asp Asn Tyr Val Gly Ser Thr  
100 105 110

Pro Ser Leu Tyr Ile Trp Asn Asp Met Asn Glu Pro Ser Val Phe Asn  
115 120 125

Gly Pro Glu Val Thr Met Pro Arg Asp Ala Leu His Val Gly Gly Val  
130 135 140

Glu His Arg Glu Leu His Asn Ala Tyr Gly Tyr Tyr Phe His Met Ala  
145 150 155 160

Thr Ala Glu Gly Leu Leu Lys Arg Gly Asp Gly Lys Asp Arg Pro Phe  
165 170 175

Val Leu Ser Arg Ala Phe Phe Ala Gly Ser Gln Arg Tyr Gly Ala Val  
180 185 190

Trp Thr Gly Asp Asn Ser Ala Asp Trp Asp His Leu Arg Val Ser Val  
195 200 205

Pro Met Val Leu Thr Leu Gly Leu Thr Gly Met Thr Phe Ser Gly Ala  
210 215 220

Asp Val Gly Gly Phe Phe Gly Asn Pro Glu Pro Glu Leu Leu Val Arg  
225 230 235 240

Trp Tyr Gln Leu Gly Ala Tyr Tyr Pro Phe Phe Arg Gly His Ala His  
245 250 255

His Asp Thr Lys Arg Arg Glu Pro Trp Leu Phe Gly Glu Arg Asn Thr  
260 265 270

Ala Leu Met Arg Asp Ala Ile Arg Ile Arg Tyr Thr Leu Leu Pro Tyr  
275 280 285

Phe Tyr Thr Leu Phe Arg Glu Ala Asn Val Ser Gly Val Pro Val Val  
 290 295 300

Arg Pro Leu Trp Met Glu Phe Pro Ser Asp Glu Ala Ala Phe Ser Asn  
 305 310 315 320

Asp Glu Ala Phe Met Val Gly Asn Ser Leu Leu Val Gln Gly Ile Tyr  
 325 330 335

Thr Ala Arg Ala Lys His Ala Ser Val Tyr Leu Pro Gly Lys Glu Ser  
 340 345 350

Trp Tyr Asp Leu Arg Thr Gly Thr Ala Tyr Lys Gly Gly Lys Val His  
 355 360 365

Lys Leu Glu Val Ser Glu Glu Ser Ile Pro Ala Phe Gln Arg Ala Gly  
 370 375 380

Thr Ile Val Pro Arg Lys Asp Arg Phe Arg Arg Ser Ser Thr Gln Met  
 385 390 395 400

Val His Asp Pro Tyr Thr Leu Val Ile Ala Leu Asn Ser Ser Gln Ala  
 405 410 415

Ala Glu Gly Glu Leu Tyr Val Asp Asp Gly Lys Ser Tyr Asp Phe Lys  
 420 425 430

His Gly Ala Tyr Ile His Arg Arg Phe Val Phe Ser Asn Gly His Leu  
 435 440 445

Thr Ser Ser Pro Val Gly Asn Ser Arg Phe Ser Ser Asp Cys Ile Ile  
 450 455 460

Glu Arg Val Ile Leu Leu Gly Phe Thr Pro Gly Ala Lys Thr Ala Leu  
 465 470 475 480

Val Glu Pro Gly Asn Gln Lys Ala Glu Ile Glu Leu Gly Pro Leu Arg  
 485 490 495

Phe Gly Gly Gln His Ala Ala Val Ala Val Thr Ile Arg Lys Pro Gly  
 500 505 510

Val Arg Val Ala Glu Asp Trp Lys Ile Lys Ile Leu  
 515 520

<210> 9

<211> 2766

<212> DNA

<213> *Arabidopsis thaliana*

<400> 9

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cgtactcccg gcgcgtgttc tctaattgtc ggcatgttt ccatcactga tggagatctc	180
gtagcgaagc ttctaccgaa agcgcctaata caaggcgatg gggatcagat caagccgttg	240
attctttctc tctcagttta caaggatggg atcgtgcggc ttaaaatcga tgaggaccat	300
tcgttgaacc cgccgaagaa gaggttccaa gttcctgatg tggtagtgtc tgagtttgag	360
gagaagaaga tctggctgca gaaagtagcg acggagacga tctctggaga cactagtccg	420
tcttcagtag tttatgtatc cgatggttac gaggcggtgg tgcgacacga tccgtttgag	480
gtgtatgtgc gtgagaaatc aggtgatcgc cgtcgcgttg tgtcattgaa ttctcatgga	540
ttatttgatt ttgagcagtt ggggaggaaa actgaaggag ataactggga agagaaattt	600
aggactcata cagattctag accatctggt cctcaatcta ttagtttcga tgtttcgttt	660
tatgattcca gtttcgttta tggaattcct gaacacgcca ctagcttcgc gttgaagcct	720
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gaatacgatc atgaatcacc gtttgggctt tacgggtcga ttccgttcat ggtttcgcat	840
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ttgtttgccca ctggttatca tcaatgtagg tggaactaca aagatgagga ggatgtggca	1140
caggtggact cgaaattcga tgaacacgat attccttatg atgttctctg gcttgacatt	1200
gagcatacag atgggaagag atactttaca tgggatagtg tgttgtttcc tcatccagag	1260

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 aaggcagaga ttgagatggg acctctgcga atgggtgggc ttgtagcttc ctcgggtaca 2700  
 aaggtgttga ctatccgcaa accgggtgtt cgagtggacc aagactggac cgtaaagatt 2760  
 ctgtga 2766

<210> 10

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> oligonucleotide PCR primer

<400> 10

ccgctcgagc gggcattttc cgcccacta

29

<210> 11

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide PCR primer

<400> 11

cgggatcccg tcacacatgg acagaagaa

29

<210> 12

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide PCR primer

<400> 12

gacggcgtct agaagattc

19

<210> 13

<211> 19

<212> DNA



<213> Artificial Sequence

<220>

<223> oligonucleotide PCR primer

<400> 13

taacttatcg ggcttctgc

19

<210> 14

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide PCR primer

<400> 14

ccctcgcttg gtacaaggta t

21

<210> 15

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide PCR primer

<400> 15

tcctgaccc ctcaccacgt a

21

<210> 16

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide PCR primer

<400> 16

cgtagtggtc tactggttca a

21

<210> 17

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide PCR primer

<400> 17

tgagctgtgt cccaagagga t

21

<210> 18

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide PCR primer

<400> 18

ggtgatgagg ataccagcga t

21

<210> 19

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide PCR primer

<400> 19

cccactccct aaccggagtt t

21

<210> 20

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide PCR primer

<400> 20

ccgctcgagc ggtttcactc acaactgtgg tctct

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<210> 21

<211> 34

<212> DNA

<213> Artificial Sequence

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34

<210> 22

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide PCR primer

<400> 22  
cgggatgaag aggatgtaga g

21

<210> 23

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide PCR primer

<400> 23  
gaaccctga gatgatccca a

21